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SEQUENCE LISTING

<110> TALL, ALAN R
WELCH, CARRIE L
LIANG, CHIEN-PING

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SUSCEPTIBILITY GENE LOCUS 2 (ATHSQ2)

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caggtatctg acctcttaaa acaataccaa gcgaacctta ctcagcagga tcgtatcctg 240

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agaagaatca gaacctccaa gaagccctgc aaagagctgc aaactcttca gaggagtccc 480

gaacctccaa gaagccctgc aaagagctgc aaactcttca gaggagtccc agagagaact 540

caagggaaag atagacacca tcacccggaa gctggacgag aaatccaaag agcaggagga 600

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1               5                  10                  15

aag tca tgt ggc aag aag cct aaa gag gag tcc cag aga gaa ctc aag        96
Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys
            20                  25                  30

gga aag ata gac acc atc acc cgg aag ctg gac gag aaa tcc aaa gag       144
Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu Lys Ser Lys Glu
        35                  40                  45

cag gag gag ctt ctg cag atg att cag aac ctc caa gaa gcc ctg cag       192
Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln
    50                  55                  60

aga gct gca aac tct tca gag gag tcc cag aga gaa ctc aag gga aag       240
Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys
65                  70                  75                  80

ata gac acc ctc acc ttg aag ctg aac gag aaa tcc aaa gag cag gag       288
Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu
                85                  90                  95

gag ctt cta cag aag aat cag aac ctc caa gaa gcc ctg caa aga gct       336
Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala
            100                 105                 110

gca aac ttt tca ggt cct tgt cca caa gac tgg ctc tgg cat aaa gaa       384
Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu
        115                 120                 125

aac tgt tac ctc ttc cat ggg ccc ttt ggc tgg gaa aaa aac cgg cag       432
Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln
    130                 135                 140

acc tgc caa tct ttg ggt ggc cag tta cta caa att aat ggt gca gat       480
Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly Ala Asp
145                 150                 155                 160

gat ctg aca ttc atc tta caa gca att tcc cat acc acc tcc cca ttc       528
Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe
                165                 170                 175

tgg att gga ttg cat cgg aag aag cct ggc caa cca tgg cta tgg gag       576
Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu
            180                 185                 190

aat gga act cct ttg aat ttt caa ttc ttt aag acc agg ggc gtt tct       624
Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser
        195                 200                 205

tta cag cta tat tca tca agc aac tgt gca tac ctt caa gac gga gct       672
Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala
    210                 215                 220

gtg ttc gct gaa aac tgc att cta att gca ttc agc ata tgt cag aag       720
Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys Gln Lys
225                 230                 235                 240
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20 25 30

Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu Lys Ser Lys Glu
35 40 45

Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln
50 55 60

Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys
65 70 75 80

Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu
85 90 95

Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala
100 105 110

Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu
115 120 125

Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln
130 135 140

Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly Ala Asp
145 150 155 160

Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe
165 170 175

Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu
180 185 190

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Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser
        195                 200                 205

Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala
    210                 215                 220

Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys Gln Lys
225                 230                 235                 240

Lys Thr Asn His Leu Gln Ile
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Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1               5                   10                  15

aag tca tgt ggc aag aag cct aaa gag gag tcc cag aga gaa ctc aag      96
Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys
            20                  25                  30

gga aag ata gac acc ctc acc ttg aag ctg aac gag aaa tcc aaa gag     144
Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu
        35                  40                  45

cag gag gag ctt cta cag aag aat cag aac ctc caa gaa gcc ctg caa     192
Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln
    50                  55                  60

aga gct gca aac ttt tca ggt cct tgt cca caa gac tgg ctt tgg cat     240
Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His
65                  70                  75                  80

aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa aaa aac     288
Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu Lys Asn
                85                  90                  95

cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att aat ggt     336
Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly
            100                 105                 110

gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc acc tcc     384
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```
Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser
        115                 120                 125

cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca tgg cta      432
Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu
    130                 135                 140

tgg gag aat gga act cct ttg aat ttt caa ttc ttt aag acc agg ggc      480
Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly
145                 150                 155                 160

gtt tct tta cag cta tat tca tca ggc aac tgt gca tac ctt caa gac      528
Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu Gln Asp
                165                 170                 175

gga gct gtg ttc gct gaa aac tgc att cta att gca ttc agc ata tgt      576
Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys
            180                 185                 190

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Gln Lys Lys Thr Asn His Leu Gln Ile
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Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys
            20                  25                  30

Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu
        35                  40                  45

Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln
    50                  55                  60

Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His
65                  70                  75                  80

Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu Lys Asn
                85                  90                  95

Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly
            100                 105                 110
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Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser
      115                 120                 125

Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu
    130                 135                 140

Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly
145                 150                 155                 160

Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu Gln Asp
            165                 170                 175

Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys
        180                 185                 190

Gln Lys Lys Thr Asn His Leu Gln Ile
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1               5                   10                  15

aag tca tgt ggc aag aag cct aaa ggt cct tgt cca caa gac tgg ctc      96
Lys Ser Cys Gly Lys Lys Pro Lys Gly Pro Cys Pro Gln Asp Trp Leu
            20                  25                  30

tgg cat aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa     144
Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu
        35                  40                  45

aaa aac cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att     192
Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile
    50                  55                  60

aat ggt gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc     240
Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr
65                  70                  75                  80

acc tcc cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca     238
Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro
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```
                85                  90                  95

tgg cta tgg gag aat gga act cct ttg aat ttt caa ttc ttt aag acc      336
Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr
            100                 105                 110

agg ggc gtt tct tta cag cta tat tca tca ggc aac tgt gca tac ctt      384
Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu
        115                 120                 125

caa gac gga gct gtg ttc gct gaa aac tgc att cta att gca ttc agc      432
Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser
    130                 135                 140

ata tgt cag aag aag aca aat cat ttg caa att tag                     468
Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile
145                 150                 155
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<212> PRT
<213> Murinae gen. sp.

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<223> Isoform 9

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Lys Ser Cys Gly Lys Lys Pro Lys Gly Pro Cys Pro Gln Asp Trp Leu
            20                  25                  30

Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu
        35                  40                  45

Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile
    50                  55                  60

Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr
65                  70                  75                  80

Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro
                85                  90                  95

Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr
            100                 105                 110

Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu
        115                 120                 125

Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser
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130 135 140

Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile
145 150 155

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Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1               5                  10                  15

aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca        96
Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
            20                  25                  30

tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg       144
Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
        35                  40                  45

tca gtg acc ctt att gta cag tgg aca caa tta cgc cag gta tct gac       192
Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
    50                  55                  60

ctc tta aaa caa tac caa gcg aac ctt act cag cag gat cgt atc ctg       240
Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65                  70                  75                  80

gaa ggg cag atg tta gcc cag cag aag gca gaa aac act tca cag gaa       288
Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu
                85                  90                  95

tca aag aag gaa ctg aaa gga aag ata gac acc ctc acc cag aag ctg       336
Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
            100                 105                 110

aac gag aaa tcc aaa gag cag gag gag ctt cta cag aag aat cag aac       384
Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
        115                 120                 125

ctc caa gaa gcc ctg caa aga gct gca aac tct tca gag gag tcc cag       432
Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln
    130                 135                 140

aga gaa ctc aag gga aag ata gac acc atc acc cgg aag ctg gac gag       480
Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu
145                 150                 155                 160
```

```
aaa tcc aaa gag cag gag gag ctt ctg cag atg att cag aac ctc caa      528
Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln
                165                 170                 175

gaa gcc ctg cag aga gct gca aac tct tca gag gag tcc cag aga gaa      576
Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu
            180                 185                 190

ctc aag gga aag ata gac acc ctc acc ttg aag ctg aac gag aaa tcc      624
Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser
        195                 200                 205

aaa gag cag gag gag ctt cta cag aag aat cag aac ctc caa gaa gcc      672
Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala
    210                 215                 220

ctg caa aga gct gca aac ttt tca ggt cct tgt cca caa gac tgg ctc      720
Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu
225                 230                 235                 240

tgg cat aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa      768
Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu
                245                 250                 255

aaa aac cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att      816
Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile
            260                 265                 270

aat ggt gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc      864
Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr
        275                 280                 285

acc tcc cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca      912
Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro
    290                 295                 300

tgg cta tgg gag aat gga act cct ttg aat ttt caa ttc ttt aag acc      960
Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr
305                 310                 315                 320

agg ggc gtt tct tta cag cta tat tca tca ggc aac tgt gca tac ctt     1008
Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu
                325                 330                 335

caa gac gga gct gtg ttc gct gaa aac tgc att cta att gca ttc agc     1056
Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser
            340                 345                 350

ata tgt cag aag aag aca aat cat ttg caa att tag                    1092
Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile
        355                 360
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<221> misc_feature
<223> Isoform 1

<400> 20

Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
20 25 30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
50 55 60

Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65 70 75 80

Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu
85 90 95

Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
100 105 110

Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
115 120 125

Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln
130 135 140

Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu
145 150 155 160

Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln
165 170 175

Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu
180 185 190

Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser
195 200 205

Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala
210 215 220

Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu
225 230 235 240

Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu

245 250 255

Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile
260 265 270

Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr
275 280 285

Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro
290 295 300

Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr
305 310 315 320

Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu
325 330 335

Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser
340 345 350

Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile
355 360

<210> 21
<211> 773
<212> DNA
<213> Murinae gen. sp.

<220>
<221> CDS
<222> (1)..(174)
<223>

<220>
<221> misc_feature
<223> Isoform 2

<400> 21
atg act ttt gat gac aag atg aag cct gcg aat gac gag cct gat cag 48
Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96
Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
20 25 30

tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg 144
Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

tca gtg acc ctt att gta cag tgg aca caa tgatcgtatc ctggaagggc 194
Ser Val Thr Leu Ile Val Gln Trp Thr Gln
50 55

agatgttagc ccagcagaag gcagaaaaca cttcacagga atcaaagaag gaactgaaag 254

gaaagataga caccctcacc cagaagctga acgagaaatc caaagagcag gaggagcttc 314

tacagaagaa tcagaacctc caagaagccc tgcaaagagc tgcaaactct tcagaggagt 374

cccagagaga actcaaggga aagatagaca ccatcacccg gaagctggac gagaaatcca 434

aagagcagga ggagcttctg cagatgattc agaacctcca agaagccctg cagagagctg 494

caaactcttc agaggagtcc cagagagaac tcaagggaaa gatagacacc ctcaccttga 554

agctgaacga gaaatccaaa gagcaggagg agcttctaca gaagaatcag aacctccaag 614

aagccctgca aagagctgca aacttttcag gtccttgtcc acaagactgg ctctggcata 674

aagaaaactg ttacctcttc cgtgggccct ttactgggaa aaaagccggc agacctgcca 734

atctttgggt ggcagttact acaaattaat gggcagatg 773

<210> 22
<211> 58
<212> PRT
<213> Murinae gen. sp.

<220>
<221> misc_feature
<223> Isoform 2

<400> 22

Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
20 25 30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln
50 55

<210> 23
<211> 495
<212> DNA
<213> Murinae gen. sp.

<220>
<221> CDS
<222> (1)..(495)
<223>

<220>
<221> misc_feature
<223> Isoform 3

<400> 23
atg act ttt gat gac aag atg aag cct gcg aat gac gag cct gat cag 48
Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96
Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
20 25 30

tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg 144
Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

tca gtg acc ctt att gta cag tgg aca caa tta cgc cag gta tct gac 192
Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
50 55 60

ctc tta aaa caa tac caa gcg aac ctt act cag cag gat cgt atc ctg 240
Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65 70 75 80

gaa ggg cag atg tta gcc cag cag aag gca gaa aac act tca ccg caa 288
Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Pro Gln
85 90 95

tca aag aag gaa ctg aaa gga aag ata gac acc ctc acc cag aag ctg 336
Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
100 105 110

aac gag aaa tcc aaa gag cag gag gag ctt cta cag aag aat cag aac 384
Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
115 120 125

ctc caa gaa gcc ctg caa aga gct gca aac tct tca gag gag tcc cag 432
Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln
130 135 140

aga gaa ctc aag gga aag ata gac acc ctc acc ttg aag ctg aac gag 480
Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu
145 150 155 160

aaa tcc aaa gag cag 495
Lys Ser Lys Glu Gln
165

<210> 24
<211> 165
<212> PRT
<213> Murinae gen. sp.

<220>
<221> misc_feature
<223> Isoform 3

<400> 24

Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
20 25 30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
50 55 60

Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65 70 75 80

Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Pro Gln
85 90 95

Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
100 105 110

Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
115 120 125

Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln
130 135 140

Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu
145 150 155 160

Lys Ser Lys Glu Gln
165

<210> 25
<211> 621
<212> DNA
<213> Murinae gen. sp.

<220>
<221> CDS
<222> (1)..(621)
<223>

<220>
<221> misc_feature
<223> Isoform 4

<400> 25
atg act ttt gat gac aag atg aag cct gcg aat gac gag cct gat cag 48
Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1 5 10 15

aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96
Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro

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            20                  25                  30

tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg      144
Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
        35                  40                  45

tca gtg acc ctt att gta cag tgg aca caa tta cgc cag gta tct gac      192
Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
    50                  55                  60

ctc tta aaa caa tac caa gcg aac ctt act cag cag gat cgt atc ctg      240
Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65                  70                  75                  80

gaa ggg cag atg tta gcc cag cag aag gca gaa aac act tca cag gaa      288
Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu
                85                  90                  95

tca aag aag gaa ctg aaa gga aag ata gac acc ctc acc cag aag ctg      336
Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
            100                 105                 110

aac gag aaa tcc aaa gag cag gag gag ctt cta cag aag aat cag aac      384
Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
        115                 120                 125

ctc caa gaa gcc ctg caa aga gct gca aac ttt tca ggt cct tgt cca      432
Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro
    130                 135                 140

caa gac tgg ctc tgg cat aaa gaa aac tgt tac ctc ttc cat ggg ccc      480
Gln Asp Trp Leu Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro
145                 150                 155                 160

ttt agc tgg gaa aaa aac cgg cag acc tgc caa tct ttg ggt ggc cag      528
Phe Ser Trp Glu Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln
                165                 170                 175

tta cta caa att aat ggt gca gat gat ctg aca ttc atc tta caa gca      576
Leu Leu Gln Ile Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala
            180                 185                 190

att tcc cat acc acc tcc ccg ttc tgg att gga ttg cat cgg aag          621
Ile Ser His Thr Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys
        195                 200                 205
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<210> 26
<211> 207
<212> PRT
<213> Murinae gen. sp.

<220>
<221> misc_feature
<223> Isoform 4

<400> 26

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Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1               5                   10                  15

Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
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20 25 30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp
50 55 60

Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu
65 70 75 80

Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu
85 90 95

Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu
100 105 110

Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn
115 120 125

Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro
130 135 140

Gln Asp Trp Leu Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro
145 150 155 160

Phe Ser Trp Glu Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln
165 170 175

Leu Leu Gln Ile Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala
180 185 190

Ile Ser His Thr Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys
195 200 205

<210> 27
<211> 712
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<223> Isoform 5

<400> 27
atgacttttg atgacaagat gaagcctgcg aatgacgagc ctgatgagaa gtcatgtggc 60

aagaagccta aaggtctgca tttgctttct tccccatggt ggttccctgc tgctatgact 120

ctggtcatcc tctgcctggt gttgtcagtg acccttattg tacagtggac acaatgatcg 180

tatcctggaa gggcagatgt tagcccagca gaaggcagaa aacacttcac aggaatcaaa 240

gaaggaactg aaaggaaaga tagacaccct cacccagaag ctgaacgact ccaaagagca 300

ggaggagcta cacccccccc gaacctccaa gaagccctgc aaagagctgc aaactcttca 360

ggtccttgtc cacaagactg gctctggcat aaagaaaact gttacctctt ccatgggccc 420

tttagctggg aaaaaaaccg gcagacctgc caatctttgg gtgggcagtt actacaaatt 480

aatggtgcag atgatctgac attcatctta caagcaattt cccataccac ctccccttct 540

tggattggat tgcatcggaa gaagcctggc aaccatgggt atgggagaat ggacttcttt 600

gaatttttaat ttttaagaca gggcgttttt acagtttttc ataaggactt gtgatactta 660

gagggctggg ttcgttgaaa tgattctatt ggttagcatg tagaaaaaaa tt 712

<210> 28
<211> 721
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<223> Isoform 6

<400> 28
atgacttttg atgacaagat gaagcctgcg aatgacgagc ctgatcagaa gtcatgtggc 60

aagaagccta aaggtctgca tttgctttct tccccatggt ggttccctgc tgctatgact 120

ctggtcatcc tctgcctggt gttgtcagtg acccttattg tacagtggac acaataggag 180

tcccagagag aactcaaggg aaagatagac accctcacct tgaagctgaa cgagaaatcc 240

aaagagcagg aggagcttct acagaagaat cagaacctcc aagaagccct gcaaagagct 300

gcaaactttt caggtccttg tccacaagac tggctctggc ataaagaaaa ctgttacctc 360

ttccatgggc cctttagctg ggaaaaaaac cggcagacct gccaatcttt gggtggccag 420

ttactacaaa ttaatggtgc agatgatctg acattcatct tacaagcaat ttcccatacc 480

acctccccgt tctggattgg attgcatcgg aagaagcctg gccaaccatg gctatgggag 540

aatggaactc ctttgaattt tcaattcttt aagaccaggg gcgtttcttt acagctatat 600

tcatcaggca actgtgcata ccttcaagac ggactgtgtt cgctgaaaac tgcattctaa 660

ttgcattcag catatgtcaa aagaagacaa atcatttgca aatttagtga atctaaagaa 720

t 721

<210> 29
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 1 REPEAT #1

<400> 29

Glu Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu
35 40 45

<210> 30
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 1 REPEAT #2

<400> 30

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys
1 5 10 15

Leu Asp Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu
35 40 45

<210> 31
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 1 REPEAT #3

<400> 31

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly
35 40 45

<210> 32
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 3 REPEAT #1

<400> 32

Gln Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu
35 40 45

<210> 33
<211> 24
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 3 REPEAT #3 PARTIAL

<400> 33

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln
20

<210> 34
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 4 REPEAT #1

<400> 34

Glu Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly
35 40 45

<210> 35
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 7 REPEAT#2

<400> 35

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys
1 5 10 15

Leu Asp Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu
35 40 45

<210> 36
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>
<221> MISC_FEATURE
<223> ISOFORM 7 REPEAT#3

<400> 36

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly
35 40 45

<210> 37
<211> 46
<212> PRT
<213> Murinae gen. sp.

<220>

<221> MISC_FEATURE
<223> ISOFORM 8 REPEAT#3

<400> 37

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln
20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly
35 40 45

<210> 38
<211> 46
<212> PRT
<213> Homo sapiens

<400> 38

Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys
1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln Asn Leu
20 25 30

Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala
35 40 45

<210> 39
<211> 44
<212> PRT
<213> Unknown

<220>
<223> SIGNATURE SEQUENCE

<220>
<221> MISC_FEATURE
<222> (2)..(43)
<223> X = ANY AMINO ACID

<400> 39

Ser Xaa Xaa Glu Leu Lys Xaa Xaa Ile Xaa Thr Xaa Xaa Xaa Lys Leu
1 5 10 15

Xaa Glu Lys Ser Lys Glu Gln Xaa Glu Leu Xaa Xaa Xaa Xaa Xaa Asn
20 25 30

Leu Gln Glu Xaa Leu Xaa Arg Xaa Ala Asn Xaa Ser
35 40

<210> 40
<211> 44
<212> PRT
<213> Unknown

<220>
<223> SIGNATURE SEQUENCE COMMON TO MOUSE AND HUMAN

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X = E, Q, OR K

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X = N, R, OR K

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X = E OR G

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X = M OR K

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X = E OR D

<220>
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<222> (12)..(12)
<223> X = L OR I

<220>
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<222> (13)..(13)
<223> X = A OR T

<220>
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<222> (14)..(14)
<223> X = R, L, OR Q

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> X = N OR D

<220>
<221> MISC_FEATURE
<222> (24)..(24)
<223> X = M OR E

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> X = H OR L

<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> X = H OR Q

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> X = Q, K OR M

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> X = N OR I

<220>
<221> MISC_FEATURE
<222> (31)..(31)
<223> X = L OR Q

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> X = T OR A

<220>
<221> MISC_FEATURE
<222> (38)..(38)
<223> X = K OR Q

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> X = V OR A

<220>
<221> MISC_FEATURE
<222> (43)..(43)
<223> X = C,F OR S

<400> 40

Ser Xaa Xaa Glu Leu Lys Xaa Xaa Ile Xaa Thr Xaa Xaa Xaa Lys Leu
1 5 10 15

Xaa Glu Lys Ser Lys Glu Gln Xaa Glu Leu Xaa Xaa Xaa Xaa Xaa Asn
20 25 30

Leu Gln Glu Xaa Leu Xaa Arg Xaa Ala Asn Xaa Ser
35 40